

SEQUENCE LISTING

<110> Allen, Steve  
Kinney, Tony  
Miao, Gou-Hua  
Orozco, Buddy

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

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<150> 60/172929  
<151> December 21, 1999

<160> 36

<170> Microsoft Office 97

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<213> Hordeum vulgare

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<220>

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 35 40 45  
 Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu  
 50 55 60  
 Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu  
 65 70 75 80  
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu  
 85 90 95  
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys  
 100 105 110  
 Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys  
 115 120 125  
 Ala Lys Xaa Ala Gly Ser Thr Arg Phe  
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 tggagccggcccgagatnca ngccgtctac gactcaccgc tcctcgaccc 360

ggggntcagt catcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420  
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Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Glu Ala Glu  
20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa  
35 40 45

Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa  
50 55 60

Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn  
65 70 75 80

Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys  
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Gln Pro Phe Leu His Gly  
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 tatacatggcc ttgatgctgc tagcgcgaa cctgcgctcc cgccctccgccc caccgctcgc 180  
 cgccgcgcgc gngttctcggt cgccgcggc ggaggcggag agggcgataac gggacgggccc 240  
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 cctcttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360  
 gcacacttct ttcaatcaag actgggtggga tgcagtgaag attgttctta ctgtcctcaa 420  
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 ctgtcttgggn aacaaca 497

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 1 5 10 15

Pro Leu Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu  
 20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile  
 35 40 45

Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala  
 50 55 60

Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr  
 65 70 75 80

Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys  
 85 90 95

Pro Gln

<210> 7  
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<212> DNA  
<213> Zea mays

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ggccttgatg	ctgctagcgc	gcaaccctgcg	ctcccgccct	cggccaccgc	tcgcccgcgc	240
cgcggcggtc	tcgtcgcccg	cggcggaggc	ggagagggcg	atacgggacg	ggccgcggaa	300
cgactggagc	cggcccgaga	tccaggccgt	ctacgactca	ccgctcctcg	acctccttct	360
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tctttcaatc	aagactggtg	gatgcagtga	agattgttct	tactgtcctc	agtcatcaag	480
ataacaacact	ggattgaagg	cccaaaaatt	gatgaacaaa	tatgctgtct	tggaagcagc	540
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cattggcagg	aaatcaaact	tcaaccagat	tcttgaatat	gtcaaggaaa	taaggggtat	660
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cattattacc	acaagatcat	atgatgatag	actgcagact	ctttagatcg	ccgtgaaagc	840
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gatccgcatg	atcgccactg	ctcggtatcac	gatgccaaag	gcaatggta	ggctttcagc	1080
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<212> PRT  
<213> Zea mays

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 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile  
 35 40 45  
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala  
 50 55 60  
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr  
 65 70 75 80  
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys  
 85 90 95  
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met  
 100 105 110  
 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly  
 115 120 125  
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg  
 130 135 140  
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly  
 145 150 155 160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln  
 165 170 175  
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu  
 180 185 190  
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr  
 195 200 205  
 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser  
 210 215 220  
 Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg  
 225 230 235 240  
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser  
 245 250 255  
 Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp  
 260 265 270  
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala  
 275 280 285  
 Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val  
 290 295 300  
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn  
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 Asp Ala Asp Gln Ala Met Phe Lys  
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 <213> Argemone mexicana  
 <220>  
 <221> unsure  
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 gagagctcgt cttcgacctt tgattttcat ttctacattt tcttctctct catcatcttc 180  
 ttcttcttca gctgctgctg ttcaaggcaga aagaacgatt aaagaaggtc caagaaacgta 240  
 ttggagcaga gatgaaattta aatcggttta tgattctcca gttctcgatc ttctttcca 300  
 tgcagctcaa gtccatagac atgctcacaa cttcaggaa gtgcagcaat gtactttct 360  
 ctctgttaag acagggtgggt gcagtgaaga ttgttcatat tgtccacaat cttccaggta 420  
 tgacactgga gtgaaagccc aaaagctgat gaacaaggga cgcagttctg caaggaagca 480  
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<212> PRT  
 <213> Argemone mexicana

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Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ala Ala  
 20 25 30

Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp  
 35 40 45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu  
 50 55 60

Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu  
 65 70 75 80

Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu  
 85 90 95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys  
 100 105 110

Ala Gln Lys Leu Met Asn Lys  
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 <212> DNA  
 <213> Glycine max

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 gttgttgtct gttgtctctg tcgtgtctat attcgcagat ctctcaactca ttctctgttg 180  
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 gagcaccctc ccttggcg ttgcactctt cctacgcgta ttccctctgccc tcagcagctg 300  
 caattcaagc tgagagagcc atcaaagaag gacccagaaaa cgattggagc cgagaccaag 360  
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 ggagcactcg cttttgtatg ggtgctgcgt ggagggatac actaggaaga aagaccaact 660  
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 ataatcacaa tcttgacact tcaagggagt attatccaaa cataatcaca acaaggactt 840  
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<212> PRT  
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Glu Arg Ala Ile Lys Glu Gly Pro Arg Asn Asp Trp Ser Arg Asp Gln  
35 40 45  
Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly  
50 55 60  
Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys  
65 70 75 80  
Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr  
85 90 95  
Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu  
100 105 110  
Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala  
115 120 125  
Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly  
130 135 140  
Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg  
145 150 155 160  
Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln  
165 170 175  
Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn  
180 185 190  
Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr  
195 200 205  
Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile  
210 215 220  
Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp  
225 230 235 240  
Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu  
245 250 255  
Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu  
260 265 270  
Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr  
275 280 285  
Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg  
290 295 300

Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala  
305 310 315 320

Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp  
325 330 335

Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys  
340 345 350

Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys  
355 360 365

Glu Ala Ala Ser Ser Ser  
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<210> 13  
<211> 479  
<212> DNA  
<213> Glycine max

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ctaccaagaa gcactcaacg caactgaacc ccgcagcaat tggacaagag aagaatcaa 240  
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attccatata cctggggcta ttcagatgtg tacattgtt aacatcaaga cgggtggttg 360  
ctcggaggaa ttgttcttac tggcgcctaa tcatcccgct accaaaccgg tctcaaagcc 420  
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<212> PRT  
<213> Glycine max

<400> 14

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Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly  
35 40 45

Gly Cys Ser Glu  
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<212> DNA  
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<220>  
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<222> (321)

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<211> 78
<212> PRT
<213> Triticum aestivum

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<220>  
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 20 25 30  
  
 Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly  
 35 40 45  
  
 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu  
 50 55 60  
  
 Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu  
 65 70 75

<210> 17  
 <211> 1396  
 <212> DNA  
 <213> Hordeum vulgare

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 gcaagattt ttcataactgc ccacagtctt caagatacag taccggattt aaggctgaaa 420  
 aattaatgaa gaaagatgcc gtcctagaag cagctaaaaaa gccaaggag gctgggagca 480  
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 ttattggctt tggagaggcg gaggaagacc gtgttagggct gttgcataca ctggccactt 840  
 tgccaaacaca cccagagatgtt gtcctatca atgcattgtat tgctgtcaaa ggcacgcctc 900  
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 ttgtatgcc aaaggcaatg gtgagacttt cggcaggcg agtacgggttccatgccag 1020  
 agcaagctct ctgctttttt gctggggcca actcgatctt cggcgggtgaa aagcttctga 1080  
 caactgcaaa caacgactttt gatgcggacc aggcaatgtt caagatcctt ggcctgattc 1140  
 ccaaggcacc gaacttggc gatgaggagg ccaccgtggc atcatccacg gagagatgtg 1200  
 agcaagccgc ttgcgtatgaa aatgttggta tagattctcg agaccacatc cggtgcaaaa 1260  
 ctggcaccat tatctccagc tagagctttt tactgttaggg atcatgtatat tttgtactcc 1320  
 ctccgttccctt aaatataagt ctttaagcg atttcaaaaaa aaaaaaaaaa 1380  
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 <211> 405  
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 <213> Hordeum vulgare

<400> 18  
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Ser Leu Arg Ser Arg Val Arg Ser Pro Phe Ala Ser Ala Val Ser Ala  
 35 40 45

Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Ala Glu Ala Glu Arg Ala  
 50 55 60

Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala  
 65 70 75 80

Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val  
 85 90 95

His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu  
 100 105 110

Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln  
 115 120 125

Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys  
 130 135 140

Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr  
 145 150 155 160

Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr  
 165 170 175

Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly  
 180 185 190

Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu  
 195 200 205

Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr  
 210 215 220

Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp  
 225 230 235 240

Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys  
 245 250 255

Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly  
 260 265 270

Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro  
 275 280 285

Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys  
 290 295 300

Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile  
 305 310 315 320

Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe  
 325 330 335

Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile  
340 345 350

Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala  
355 360 365

Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn  
370 375 380

Phe Gly Asp Glu Glu Ala Thr Val Ala Ser Ser Thr Glu Arg Cys Glu  
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Gln Ala Ala Ser Met  
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<210> 19

<211> 1467

<212> DNA

<213> Zea mays

<400> 19

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cgcccgctgc tcctctatcc ctccctgtct gctgctacta ccttaagcta tcactatcat 180  
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acaacaagct gaagaactca agaaggctgg acttacagca tataatcata acctagatac 660  
atcaagagag tattatccca acattattac cacaagatca tatgatgata gactgcagac 720  
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<210> 20

<211> 344

<212> PRT

<213> Zea mays

<400> 20

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Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu  
20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile  
 35 40 45  
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala  
 50 55 60  
 Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met Asn  
 65 70 75 80  
 Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly Ser  
 85 90 95  
 Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys  
 100 105 110  
 Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly Met  
 115 120 125  
 Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln Ala  
 130 135 140  
 Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp  
 145 150 155 160  
 Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr Asp  
 165 170 175  
 Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser Ile  
 180 185 190  
 Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val  
 195 200 205  
 Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val  
 210 215 220  
 Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln  
 225 230 235 240  
 Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg  
 245 250 255  
 Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg  
 260 265 270  
 Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser  
 275 280 285  
 Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp  
 290 295 300  
 Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro  
 305 310 315 320  
 Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser Glu  
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 Arg Ser Glu Gln Ala Ala Ser Met  
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<210> 21  
<211> 1515  
<212> DNA  
<213> Zea mays

<400> 21

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ttaagctata	atggccttga	tgtctgtgc	ggcacacctg	cgctcccgcc	tccgcccacc	180
gctcgccgccc	gcccgcgcgt	tctcgctggc	cgccggggag	gcccggaggg	cgatacggga	240
cggggccgcgg	aacgactgga	gcccggccga	gatccaggcc	gtctacgact	caccgctcct	300
cgacccctc	tttcacgggg	ctcagggtcca	cagaaatgtc	cataaattca	gagaagtgc	360
gcaatgcaca	cttcttcaa	tcaagactgg	tggatgcagt	gaagattgtt	cttactgtcc	420
tcagtcata	agataacaaca	ctggattgaa	ggcccaaaaa	ttgatgaaca	aagatgctgt	480
cttggaaagca	gcaaaaaagg	caaaagagtc	tgggagcacc	cgtttttgca	tgggagctgc	540
atggagagaaa	accattggca	gaaaatcaa	cttcaaccag	attcttgaat	atgtcaagga	600
aataagggggt	atgggcattgg	aggctctttg	cacactaggc	atgatagaga	aacaacaaggc	660
tgaagaactc	aagaaggctg	gacttacaggc	atataatcat	aacctagata	catcaagaga	720
gtattatccc	aacattatta	ccacaagatc	atatgtatgt	agactgcaga	cttttgagca	780
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ggaggaccgg	gttaggggtgt	tgcataccct	agctacccctt	cctacacacc	cagagagcgt	900
tcctttaat	gcattggttg	ctgtaaaagg	cacacccctt	gaggaccaga	agcctgtaga	960
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gtagaatata	tacatatcat	taccgattat	ccgtatcagc	gttggggcga	aactagaact	1320
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aaaaaaaaaa	aaaaaa					1515

<210> 22  
<211> 377  
<212> PRT  
<213> Zea mays

<400> 22

Met	Ala	Leu	Met	Leu	Leu	Ala	Arg	Asn	Leu	Arg	Ser	Arg	Leu	Arg	Pro
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Arg	Ala	Ile	Arg	Asp	Gly	Pro	Arg	Asn	Asp	Trp	Ser	Arg	Pro	Glu	Ile
													35	40	45
Gln	Ala	Val	Tyr	Asp	Ser	Pro	Leu	Leu	Asp	Leu	Leu	Phe	His	Gly	Ala
													50	55	60
Gln	Val	His	Arg	Asn	Val	His	Lys	Phe	Arg	Glu	Val	Gln	Gln	Cys	Thr
												65	70	75	80
Leu	Leu	Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr	Cys
													85	90	95
Pro	Gln	Ser	Ser	Arg	Tyr	Asn	Thr	Gly	Leu	Lys	Ala	Gln	Lys	Leu	Met
												100	105		110

Asn Lys Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly  
 115 120 125

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg  
 130 135 140

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly  
 145 150 155 160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln  
 165 170 175

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu  
 180 185 190

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr  
 195 200 205

Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser  
 210 215 220

Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg  
 225 230 235 240

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser  
 245 250 255

Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp  
 260 265 270

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala  
 275 280 285

Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val  
 290 295 300

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn  
 305 310 315 320

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe  
 325 330 335

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala  
 340 345 350

Pro Ser Phe Gly Glu Glu Val Ser Ala Ala Ala Pro Ala Glu Ser  
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Glu Arg Ser Glu Gln Ala Ala Ser Met  
 370 375

<210> 23  
 <211> 1439  
 <212> DNA  
 <213> Zea mays

<400> 23  
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 gctggactta cagcatataa tcataaccta gatacatcaa gagagtatta tcccaacatt 720  
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 cattggattt tagaaaccac aacatttcat tattttgtaa ttgcttgaga ctgaatgggg 1380  
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<210> 24  
 <211> 377  
 <212> PRT  
 <213> Zea mays

<400> 24  
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 35 40 45  
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala  
 50 55 60  
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr  
 65 70 75 80  
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys  
 85 90 95  
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met  
 100 105 110  
 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly  
 115 120 125  
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg  
 130 135 140  
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly  
 145 150 155 160  
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln  
 165 170 175

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu  
180 185 190

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr  
195 200 205

Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser  
210 215 220

Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg  
225 230 235 240

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser  
245 250 255

Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp  
260 265 270

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala  
275 280 285

Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val  
290 295 300

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn  
305 310 315 320

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe  
325 330 335

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala  
340 345 350

Pro Ser Phe Gly Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser  
355 360 365

Glu Arg Ser Glu Gln Ala Ala Ser Met  
370 375

<210> 25

<211> 1477

<212> DNA

<213> Argemone mexicana

<400> 25

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1477

<210> 26

<211> 379

<212> PRT

<213> Argemone mexicana

<400> 26

Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe  
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Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ala Ala  
 20 25 30

Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp  
 35 40 45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu  
 50 55 60

Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu  
 65 70 75 80

Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu  
 85 90 95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys  
 100 105 110

Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys  
 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg  
 130 135 140

Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val  
 145 150 155 160

Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met  
 165 170 175

Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala  
 180 185 190

Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile  
 195 200 205

Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg  
 210 215 220

Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu  
225 230 235 240

Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro  
245 250 255

Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly  
260 265 270

Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg  
275 280 285

Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu  
290 295 300

Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe  
305 310 315 320

Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr  
325 330 335

Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly  
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Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu  
355 360 365

Ala Glu Arg Cys Glu Gln Glu Ala Thr Ala Ser  
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<210> 27

<211> 1526

<212> DNA

<213> Glycine max

<400> 27

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gcaactgcac gtatcgtaat gccaaaagca atggcaggat tatcagctgg cagagttcga 1140  
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gaaaagcttc tcactactcc taacaatgtat tttgatgtcg atcaactcat gttttaagtt 1260  
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ctcaacttc tctaattgct cattagcatg tactgatgtt aggtttcattt gaattttgtct 1440

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 <211> 415  
 <212> PRT  
 <213> Glycine max

<400> 28  
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Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu  
 20 25 30

Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile  
 35 40 45

Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser  
 50 55 60

Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly  
 65 70 75 80

Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser  
 85 90 95

Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala  
 100 105 110

His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr  
 115 120 125

Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr  
 130 135 140

Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu  
 145 150 155 160

Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met  
 165 170 175

Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln  
 180 185 190

Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys  
 195 200 205

Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys  
 210 215 220

Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr  
 225 230 235 240

Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr  
 245 250 255

Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile  
 260 265 270

Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr  
275 280 285

Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu  
290 295 300

Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile  
305 310 315 320

Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys  
325 330 335

Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu  
340 345 350

Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu  
355 360 365

Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met  
370 375 380

Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly  
385 390 395 400

Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser  
405 410 415

<210> 29

<211> 1659

<212> DNA

<213> Glycine max

<400> 29

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ctcttcctct gttcgctttc aagtcaaaa gtcgagaaac tatggtaccg tatcatctgt 180  
tcctccctcaa gctacagaaa catcaagcac atcacctgt aaggatgtct accaagaagc 240  
actcaacgca actgaacccc gcagcaattt gacaagagaa gaaatcaagg cgatctatga 300  
taagccattt atggagttat gttgggggtgc tggtagttt cacagggaaat tccatataacc 360  
tggggctatt cagatgtgtac tattgttgc catcaagacg gttgggtgc cggaggattt 420  
ttcttactgc gcccaatcat cccgctacca aaccggcttc aaagcctcca aaatggtctc 480  
cgtcgaatct gtcctcgccat ccgcggccat cgccaaagac aacggtagta cacgtttctg 540  
catggggatcc gctgtggcgat atatgcgtgg acgaaaaacc aatctcaaaa atgtcaaaac 600  
aatgggttagc gagattcgccg gaatgggtat ggaagtatgt gtcacgcttg gtatgattga 660  
tgcagagcaa gctcaggaaac tcaaagaago cggtcttacg gttataatc ataatgtgaa 720  
tacgtcgagg gatttcttac ccaagggtt cacgaccagg attatgtat agagatttggaa 780  
taccattaaat aatgtgagag aggccggat caatgtttgt acgggtggaa tcctcggtt 840  
aggagaaaat aagtctgacc atattggact tttggagacg gttgctacgt tgccttcgca 900  
tccggaaatca tttccctgtgtac acatgttagt ggctatcaaa ggaacaccac tggaaaggaaa 960  
caagaagggtg gaatttgaga atatgttgcg aatgggttgcg acggcttagaa tcgtcatgcc 1020  
taaaaccatc gtgcgtttgg cagctggaaag aggagaattt agcgaggaaac aacagggttt 1080  
atgtttcatg gccggagccat atgcccgtttt cacaggagaa acaatgttacccacaccaggc 1140  
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ggttttgtttt gatgtgagag aatgattgtt tagaaggaaa gaatgtatatacggaaacagt 1560

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 <211> 417  
 <212> PRT  
 <213> Glycine max

<400> 30  
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Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln  
 20 25 30

Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln  
 35 40 45

Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu  
 50 55 60

Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile  
 65 70 75 80

Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly  
 85 90 95

Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr  
 100 105 110

Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys  
 115 120 125

Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val  
 130 135 140

Ser Val Glu Ser Val Leu Ala Ala Arg Ile Ala Lys Asp Asn Gly  
 145 150 155 160

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg  
 165 170 175

Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly  
 180 185 190

Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln  
 195 200 205

Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val  
 210 215 220

Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr  
 225 230 235 240

Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn  
 245 250 255

Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His  
 260 265 270

Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser  
275 280 285

Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly  
290 295 300

Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala  
305 310 315 320

Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly  
325 330 335

Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn  
340 345 350

Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp  
355 360 365

Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu  
370 375 380

Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn  
385 390 395 400

Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val  
405 410 415

Ala

<210> 31

<211> 1032

<212> DNA

<213> Triticum aestivum

<400> 31

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tttgcattggg agccgcattgg agagagacaa ttggcaggaa aacaaatttc aaccagattc 120  
ttgaatatgt caaggacata agaggatgg gcatggaggt ctgttgccacc ctgggcatgc 180  
tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240  
tagatacatac aagagaatat taccctaaca ttatttctac aagatcgatc gatgatagat 300  
tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcaggt ggaatttattg 360  
gtcttggaga ggcggaggaa gaccgtgttag ggctgttgca tacactggcc actttgccaa 420  
cacaccaga gagcgttccct atcaatgtat tgattgtgt caaaggcacc cctttcagg 480  
atcagaagcc tgttagagata tggaaatgat tccgcattgtat tgccagcgcgc cggatttgta 540  
tgccaaaggc aatgggtgaga ctttcggcag ggagagatcg gttttccatcg ccagaacaag 600  
ctctctgtt tctcgctggg gccaactcga tcttcggccgg tggaaagctc ctgacaactg 660  
cgaacaatga ctttgatgcg gaccaggcaa tggtaagat ctttggctgtt attcccaagg 720  
ctccaaactt tggcgatgaa gaggtcatgg tagcagcacc cacggagaga tgtgagcaag 780  
ccgccttgcgt gtaaaatgtc ggtatagatt ctcgagatca catccggcgc aaaactggca 840  
ccattatctc cacctagagt tttgtactgt agagatcatg acattttata gtaacttcag 900  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020  
aaaaaaaaaa aa 1032

<210> 32

<211> 263

<212> PRT

<213> Triticum aestivum

<400> 32

Thr	Arg	Asp	Ala	Val	Leu	Glu	Ala	Ala	Lys	Lys	Ala	Lys	Glu	Ala	Gly
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Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg

20					25					30					
----	--	--	--	--	----	--	--	--	--	----	--	--	--	--	--

Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly

35				40					45						
----	--	--	--	----	--	--	--	--	----	--	--	--	--	--	--

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln

50			55			60									
----	--	--	----	--	--	----	--	--	--	--	--	--	--	--	--

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu

65			70			75			80						
----	--	--	----	--	--	----	--	--	----	--	--	--	--	--	--

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr

85				90			95								
----	--	--	--	----	--	--	----	--	--	--	--	--	--	--	--

Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser

100				105			110								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg

115			120			125									
-----	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--	--

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser

130			135			140									
-----	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--	--

Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp

145			150			155			160						
-----	--	--	-----	--	--	-----	--	--	-----	--	--	--	--	--	--

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala

165				170			175								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val

180				185			190								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn

195				200			205								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe

210			215			220									
-----	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--	--

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala

225			230			235			240						
-----	--	--	-----	--	--	-----	--	--	-----	--	--	--	--	--	--

Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg

245				250			255								
-----	--	--	--	-----	--	--	-----	--	--	--	--	--	--	--	--

Cys Glu Gln Ala Ala Leu Met

260															
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<210> 33  
<211> 378  
<212> PRT  
<213> *Arabidopsis thaliana*

<400> 33

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1			5			10				15					

Ser Gly Gly Leu Gln Ser Ala Ser Cys Tyr Ser Ser Leu Ser Ala Ala  
 20 25 30

Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp  
 35 40 45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu  
 50 55 60

Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu  
 65 70 75 80

Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu  
 85 90 95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys  
 100 105 110

Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys  
 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg  
 130 135 140

Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile  
 145 150 155 160

Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met  
 165 170 175

Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala  
 180 185 190

Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile  
 195 200 205

Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg  
 210 215 220

Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu  
 225 230 235 240

Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro  
 245 250 255

Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly  
 260 265 270

Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg  
 275 280 285

Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu  
 290 295 300

Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe  
 305 310 315 320

Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr  
 325 330 335

Pro	Asn	Asn	Asp	Phe	Asp	Ala	Asp	Gln	Leu	Met	Phe	Lys	Thr	Leu	Gly
340								345						350	
Leu	Ile	Pro	Lys	Pro	Pro	Ser	Phe	Ser	Glu	Asp	Asp	Ser	Glu	Ser	Glu
355							360					365			
Asn	Cys	Glu	Lys	Val	Ala	Ser	Ala	Ser	His						
370						375									
<210>	34														
<211>	363														
<212>	PRT														
<213>	Schizosaccharomyces pombe														
<400>	34														
Met	Phe	Thr	Arg	Thr	Ile	Arg	Gln	Gln	Ile	Arg	Arg	Ser	Ser	Ala	Leu
1					5					10				15	
Ser	Leu	Val	Arg	Asn	Asn	Trp	Thr	Arg	Glu	Glu	Ile	Gln	Lys	Ile	Tyr
20							25						30		
Asp	Thr	Pro	Leu	Ile	Asp	Leu	Ile	Phe	Arg	Ala	Ala	Ser	Ile	His	Arg
35							40						45		
Lys	Phe	His	Asp	Pro	Lys	Lys	Val	Gln	Gln	Cys	Thr	Leu	Leu	Ser	Ile
50							55					60			
Lys	Thr	Gly	Gly	Cys	Thr	Glu	Asp	Cys	Lys	Tyr	Cys	Ala	Gln	Ser	Ser
65							70			75			80		
Arg	Tyr	Asn	Thr	Gly	Val	Lys	Ala	Thr	Lys	Leu	Met	Lys	Ile	Asp	Glu
					85				90				95		
Val	Leu	Glu	Lys	Ala	Lys	Ile	Ala	Lys	Ala	Lys	Gly	Ser	Thr	Arg	Phe
					100			105					110		
Cys	Met	Gly	Ser	Ala	Trp	Arg	Asp	Leu	Asn	Gly	Arg	Asn	Arg	Thr	Phe
						115		120				125			
Lys	Asn	Ile	Leu	Glu	Ile	Ile	Lys	Glu	Val	Arg	Ser	Met	Asp	Met	Glu
						130		135				140			
Val	Cys	Val	Thr	Leu	Gly	Met	Leu	Asn	Glu	Gln	Gln	Ala	Lys	Glu	Leu
145						150			155				160		
Lys	Asp	Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	Asp	Thr	Ser	Arg
						165			170				175		
Glu	Tyr	Tyr	Ser	Lys	Ile	Ile	Ser	Thr	Arg	Thr	Tyr	Asp	Glu	Arg	Leu
						180		185				190			
Asn	Thr	Ile	Asp	Asn	Leu	Arg	Lys	Ala	Gly	Leu	Lys	Val	Cys	Ser	Gly
						195			200			205			
Gly	Ile	Leu	Gly	Leu	Gly	Glu	Lys	Lys	His	Asp	Arg	Val	Gly	Leu	Ile
						210		215				220			
His	Ser	Leu	Ala	Thr	Met	Pro	Thr	His	Pro	Glu	Ser	Val	Pro	Phe	Asn
						225		230			235			240	

Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu  
 245 250 255  
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile  
 260 265 270  
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys  
 275 280 285  
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val  
 290 295 300  
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser  
 305 310 315 320  
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe  
 325 330 335  
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro  
 340 345 350  
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu  
 355 360  
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 <211> 375  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*  
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 Thr Lys Tyr Ala Thr Asn Ala Ala Val Lys Ser Thr Thr Ala Ser Ser  
 20 25 30  
 Glu Ala Ser Thr Leu Gly Ala Leu Gln Tyr Ala Leu Ser Leu Asp Glu  
 35 40 45  
 Pro Ser His Ser Trp Thr Lys Ser Gln Leu Lys Glu Ile Tyr His Thr  
 50 55 60  
 Pro Leu Leu Glu Leu Thr His Ala Ala Gln Leu Gln His Arg Lys Trp  
 65 70 75 80  
 His Asp Pro Thr Lys Val Gln Leu Cys Thr Leu Met Asn Ile Lys Ser  
 85 90 95  
 Gly Gly Cys Ser Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser Arg Asn  
 100 105 110  
 Asp Thr Gly Leu Lys Ala Glu Lys Met Val Lys Val Asp Glu Val Ile  
 115 120 125  
 Lys Glu Ala Glu Glu Ala Lys Arg Asn Gly Ser Thr Arg Phe Cys Leu  
 130 135 140  
 Gly Ala Ala Trp Arg Asp Met Lys Gly Arg Lys Ser Ala Met Lys Arg  
 145 150 155 160

Ile	Gln	Glu	Met	Val	Thr	Lys	Val	Asn	Asp	Met	Gly	Leu	Glu	Thr	Cys
165							170						175		
Val	Thr	Leu	Gly	Met	Val	Asp	Gln	Asp	Gln	Ala	Lys	Gln	Leu	Lys	Asp
180							185						190		
Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Ile	Asp	Thr	Ser	Arg	Glu	His
195							200						205		
Tyr	Ser	Lys	Val	Ile	Thr	Thr	Arg	Thr	Tyr	Asp	Asp	Arg	Leu	Gln	Thr
210							215						220		
Ile	Lys	Asn	Val	Gln	Glu	Ser	Gly	Ile	Lys	Ala	Cys	Thr	Gly	Gly	Ile
225							230						235		240
Leu	Gly	Leu	Gly	Glu	Ser	Glu	Asp	Asp	His	Ile	Gly	Phe	Ile	Tyr	Thr
245							250						255		
Leu	Ser	Asn	Met	Ser	Pro	His	Pro	Glu	Ser	Leu	Pro	Ile	Asn	Arg	Leu
260							265						270		
Val	Ala	Ile	Lys	Gly	Thr	Pro	Met	Ala	Glu	Glu	Leu	Ala	Asp	Pro	Lys
275							280						285		
Ser	Lys	Lys	Leu	Gln	Phe	Asp	Glu	Ile	Leu	Arg	Thr	Ile	Ala	Thr	Ala
290							295						300		
Arg	Ile	Val	Met	Pro	Lys	Ala	Ile	Ile	Arg	Leu	Ala	Ala	Gly	Arg	Tyr
305							310						315		320
Thr	Met	Lys	Glu	Thr	Glu	Gln	Phe	Val	Cys	Phe	Met	Ala	Gly	Cys	Asn
							325						330		335
Ser	Ile	Phe	Thr	Gly	Lys	Lys	Met	Leu	Thr	Thr	Met	Cys	Asn	Gly	Trp
							340						345		350
Asp	Glu	Asp	Lys	Ala	Met	Leu	Ala	Lys	Trp	Gly	Leu	Gln	Pro	Met	Glu
							355						360		365
Ala	Phe	Lys	Tyr	Asp	Arg	Ser									
							370						375		
<210>	36														
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<213>															
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